

SEQUENCE LISTING

<110> Kufer Dr, Peter

<120> A novel method of identifying binding site domains that
retain the capacity of binding to an epitope

<130> B 3077 PCT

<150> EP 97 12 0096.9

<151> 1997-11-17

<160> 75

<170> PatentIn Ver. 2.0

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29

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<211> 22

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<400> 12

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22

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SEQUENCE LISTING

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17

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38

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ctagtgtat ggtgatggtg atgg

24

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gggtgggtctg agctcgaaa 79

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<400> 23

gcctccggaa gcattgacag gaggttgagg 30

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<211> 33

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32

<210> 27

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<212> DNA

<213> Artificial Sequence

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30

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<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 28

aatctagaac catggttgct gggagcgacg

30

<210> 29

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<212> DNA

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32

<210> 30

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<212> DNA

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<400> 30

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32

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<400> 32

saggtgcagc tcgaggagtc aggacct

27

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gaggtccagc tcgagcagtc tggacct

27

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<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 35

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<210> 36

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 36

gargtgaagc tcgaggaggatc tggagga

27

<210> 37

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 37

gaggtaaagc ttctcgagtc tggaggt

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<210> 38

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

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gaagttaaagc tcgaggagtc tggggga

27

<210> 39

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 39

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27

<210> 40

<211> 34

<212> DNA

<213> Artificial Sequence

SEARCHED
INDEXED
MAILED
1999-03-09
10:00:00

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<400> 40

tgaggagacg gtgaccgtgg tcccttggcc ccag

34

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<211> 32

<212> DNA

<213> Artificial Sequence

<220>

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<400> 42

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32

<210> 43

17/48

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 43

ccagttccga gctcgtgctc acccagtctc ca

32

<210> 44

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> synthetic oligonucleotide

<400> 44

ccagttccga gctccagatg acccagtctc ca

32

<210> 45

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 45

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31

<210> 46

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 46

ccagatgtga gctcgtcatg acccagtctc ca

32

<210> 47

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 47

ccagttccga gctcgtgatg acacagtctc ca

32

<210> 48

<211> 39

<212> DNA

<213> Artificial Sequence

19/48

<220>

<223> synthetic oligonucleotide

<400> 48

tggtgcacta gtcgtacgtt tgatctcaag cttggtccc

39

<210> 49

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

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cattgag

67

<210> 50

<211> 42

<212> DNA

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<220>

<223> synthetic oligonucleotide

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<210> 51

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 51

gatccaccac cgccctgaacc tccaccccccgaaccaccac ct

42

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<211> 14

<212> PRT

<213> Artificial Sequence

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<223> peptide encoded by synthetic oligonucleotide

<400> 52

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly

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5

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<210> 53

<211> 381

<212> DNA

<213> Homo sapiens

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tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

21/48

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gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatatg 300
gggtggggca gtggctggag accctactac tactacggta tggacgtctg gggccaagg 360
accacggtca ccgtctccctc a 381

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<211> 127

<212> PRT

<213> Homo sapiens

<400> 54

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

22/48

Ala Lys Asp Met Gly Trp Gly Ser Gly Trp Arg Pro Tyr Tyr Tyr Tyr

100

105

110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115

120

125

<210> 55

<211> 321

<212> DNA

<213> Homo sapiens

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ggacagcctc ctaagctgct catttactgg gcatctaccc gggaatccgg ggtccctgac 180

cgattcagtg gcagcgggtc tgggacagat ttcactctca ccatcagcag tctacaacct 240

gaagattctg caacttacta ctgtcagcag agttacgaca tcccgtacac ttttgccag 300

gggaccaagc tggagatcaa a 321

<210> 56

<211> 107

<212> PRT

<213> Homo sapiens

<400> 56

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1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile

35 40 45

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Ile Pro Tyr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 57

<211> 201

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 57

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24/48

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ggccgctcta gagtcgacct c 201

<210> 58

<211> 525

<212> DNA

<213> M13-Phage and artificial sequence of the MCS

<220>

<223> DNA-sequence of the N2-domain and the MCS

<400> 58

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acttatatatca accctctcgat cggcacttat ccgcctggta ctgagcaaaa ccccgctaatt 120
cctaattcattt ctcttgagga gtctcagcct cttaataactt tcatgtttca gaataatagg 180
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cccgtaaaaa cttattacca gtacactcct gtatcatcaa aagccatgta tgacgcttac 300
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ggtgatccg aggtgcagct gctcgagccc ggtcaccgtc tcctcaggtg gtgggtggttc 480
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<210> 59

<211> 137

<212> PRT

<213> Artificial Sequence

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<223> protein sequence M13 protein III and N2-domain

<400> 59

Thr Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr

1 5 10 15

Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro

20 25 30

Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe

35 40 45

Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val

50 55 60

Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr

65 70 75 80

Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn

85 90 95

Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro

100 105 110

Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro

115 120 125

Val Asn Ala Ser Gly Gly Gly Ser

130 135

<210> 60

<211> 726

<212> DNA

<213> Mus sp.

<400> 60

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tacaatgaga gtttcagggg caaagccaca ctgactgcag acaaattcctc gagcacagcc 240
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ggatctggta cagatttac tctcaccatc agtagcctgg agcctgaaga ttttgcata 660
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atcaaa 726

<210> 61

<211> 242

<212> PRT

<213> Mus sp.

<400> 61

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly

27/48

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn

20

25

30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp

35

40

45

Ile Gly Asp Leu Phe Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg

50

55

60

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala

65

70

75

80

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

85

90

95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser

130

135

140

Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala

145

150

155

160

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly

165

170

175

Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly

180 185 190

Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln

210 215 220

Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu

225 230 235 240

Ile Lys

<210> 62

<211> 753

<212> DNA

<213> Mus sp.

<400> 62

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ctcgtgatga cccagactcc actctccctg cctgtcagtc ttggagatca agcctccatc 480
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<210> 63

<211> 251

<212> PRT

<213> Mus sp.

<400> 63

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1 5 10 15

Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
20 25 30

Tyr Gly Leu Ser Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp
35 40 45

Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

30/48

85

90

95

Cys Ala Arg Arg Gly Ser Tyr Gly Ser Asn Tyr Asp Trp Tyr Phe Asp

100

105

110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly

115

120

125

Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Leu Val Met Thr

130

135

140

Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile

145

150

155

160

Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr

165

170

175

Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

180

185

190

Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly

195

200

205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala

210

215

220

Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr

225

230

235

240

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys

245

250

<210> 64

<211> 726

<212> DNA

<213> Mus sp.

<400> 64

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cttcttatct actctggatc cactttgcaa tctggaaattc catcaagggtt cagtggcagt 600
ggatctggta cagatttcac tctcaccatc agtagcctgg agcctgaaga ttttgcataatg 660
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atcaaa 726

<210> 65

<211> 242

<212> PRT

<213> Mus sp.

<400> 65

32/48

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Ala Leu Val Arg Pro Gly

1

5

10

15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn

20

25

30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp

35

40

45

Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg

50

55

60

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala

65

70

75

80

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

85

90

95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Ser Gly Glu Leu Gln Met Thr Gln Ser Pro Ser

130

135

140

Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala

145

150

155

160

33/48

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly

165

170

175

Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly

180

185

190

Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln

210

215

220

Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu

225

230

235

240

Ile Lys

<210> 66

<211> 744

<212> DNA

<213> Mus sp.

<400> 66

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctggac ttcagtgaag 60

atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggttaagcag 120

aggcctggac atggacttga atgggttgg aatatttcc ctggaagtgg taatgctcac 180

tacaatgaga agttcaaggg caaagccaca ctgactgcag acaagtccctc gtacacagcc 240

tatatgcagc tcagtagcct gacatctgag gactctgctg tctatttctg tgcaagattg 300

cggaactggg acgaggctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtgtggtg gttctggcg cgccggctcc ggtgggttg gttctgagct cgtgatgaca 420
cagtctccat cctccctgag tgtgtcagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgtaaacag tggaaatcaa aagaactact tggcctggta ccagcagaaa 540
ccagggcagc ctcctaaact gttgatctac ggggcatcca ctaggaaatc tggggccct 600
gatcgcttca caggcagttg atctggaaca gatttcactc tcaccatca gagtgtgcag 660
gctgaagacc tggcagtttta ttactgtcag aatgattata gttatccgta cacgttcgga 720
ggggggacca agcttgagat caaa 744

<210> 67

<211> 248

<212> PRT

<213> Mus sp.

<400> 67

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly

1

5

10

15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn

20

25

30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp

35

40

45

Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys

50

55

60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala

65

70

75

80

Gly Gly Thr Lys Leu Glu Ile Lys

245

<210> 68

<211> 726

<212> DNA

<213> Mus sp.

<400> 68

gaggtgcagc tgctcgagca gtctggagct gagctggta ggcctggggc ttca
atatcctgca aggcttctgg atacgccttc aataactact ggcttaggttg ggtaa
aggcctggac atggacttga gtggatttga gacatttacc ctgaaagtgg aaata
tacaatgaga ggttcagggg caaagccaca ctgactgcag acaaattcctc gag
tttatgcagt taagtagcct gacatctgag gactctgctg tctatttctg tgca
aggaactggg acgaggctat ggactactgg ggccaaggga ccacggcac
cgtctccat cttatcttgc tgcatctcct ggagaaacca ttactattaa ttgc
agtaagagca ttagcaaata tttagcctgg tatcaagaga aacctggaa aact
cttcttatct actctggatc cactttgcaa tctggaattc catcaagg
ggatctggta cagatttcac tctcaccatc agtagcctgg agcctgaaga
tattactgtc aacagcataa tgaatacccg tacacgttcg gaggggggac
atcaaa 726

<210> 69

<211> 242

<212> PRT

<213> Mus sp.

37/48

<400> 69

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly

1

5

10

15

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Asn Asn

20

25

30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp

35

40

45

Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg

50

55

60

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala

65

70

75

80

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

85

90

95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser

130

135

140

Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala

145

150

155

160

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly

165

170

175

Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly

180

185

190

Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln

210

215

220

Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu

225

230

235

240

Ile Lys

<210> 70

<211> 753

<212> DNA

<213> Mus sp.

<400> 70

gaggtgcagc tgctcgagca gtctggagct gagctggcga ggcctgggc ttcagtgaag 60
ctgtcctgca aggcttctgg ctacaccctc acaaactatg gtttaagctg ggtgaagcag 120
aggcctggac aggtccttga gtggattgga gaggtttatc ctagaattgg taatgcttac 180

39/48

tacaatgaga agttcaaggg caaggccaca ctgactgcag acaaattcctc cagcacagcg 240
tccatggagc tccgcagcct gacctctgag gactctgcgg tctatttctg tgcaagacgg 300
ggatcctacg atactaacta cgactggtac ttcgatgtct gggccaagg gaccacggc 360
accgtctcct caggtggtgg tggttctggc ggccggcggtc ccggtggtgg tggttctgag 420
ctcgtgatga cccagactcc actctccctg cctgtcagtc ttggagatca agcctccatc 480
tcttgcagat ctagtcagag cttgtacac agtaatggaa acacctattt acattggtac 540
ctgcagaagc caggccagtc tccaaagctc ctgatctaca aagtttccaa ccgattttct 600
ggggtcccag acaggttcag tggcagtggc tcagggacag atttcacact caagatcagc 660
agagtggagg ctgaggatct gggagttat ttctgctctc aaagtacaca tggccgtac 720
acgttcggag gggggaccaa gcttgagatc aaa 753

<210> 71

<211> 251

<212> PRT

<213> Mus sp.

<400> 71

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly

1

5

10

15

Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn

20

25

30

Tyr Gly Leu Ser Trp Val Lys Gln Arg Pro Gly Gln Val Leu Glu Trp

35

40

45

Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys

50

55

60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala

40/48

65

70

75

80

Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

85

90

95

Cys Ala Arg Arg Gly Ser Tyr Asp Thr Asn Tyr Asp Trp Tyr Phe Asp

100

105

110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly

115

120

125

Ser Gly Gly Gly Ser Gly Gly Ser Glu Leu Val Met Thr

130

135

140

Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile

145

150

155

160

Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr

165

170

175

Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

180

185

190

Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly

195

200

205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala

210

215

220

41/48

Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr

225

230

235

240

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys

245

250

<210> 72

<211> 717

<212> DNA

<213> Mus sp.

<400> 72

gaggtgcagc tgctcgagtc tggaggtggc ctgggtgcagc ctggaggatc cctgaaactc 60
tcctgtgcag cctcaggatt cgattttagt agatactgga tgagttgggt ccggcaggct 120
ccagggaaag ggctagaatg gattggagaa attaatccag atagcagttac gataaactat 180
acgccatctc tgaaggataa attcatcatc tccagagaca acgccaaaaa tacgctgtac 240
ctgcaaatgg gcaaagttag atctgaggac acagcccttt attactgtgc aagaggagcc 300
ttcccttttg actactgggg ccaagggacc acggtcaccc ttccttcagg tggtggttgt 360
tctggcggcg gcccgtccgg tggtggttgt tctgagctcg tgctcaccca gtctccaacc 420
accatggctg catctcccg ggagaagatc actatcacct gcagtgcacag ctcaagtata 480
agttccaatt acttgcattt gatatcagcag aagccaggat tctccctaa actcttgatt 540
tataggacat ccaatctggc ttctggagtc ccagctcgct tcagtgccag tgggtctggg 600
acctcttact ctctcacaat tggcaccatg gaggctgaag atgttgccac ttactactgc 660
cagcagggta gtagtataacc actcacgttc ggtgctggga ccaagcttga gatcaaa 717

<210> 73

<211> 239

<212> PRT

<213> Mus sp.

<400> 73

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu
50 55 60

Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Gly Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Gly Ala Phe Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Glu Leu Val Leu Thr Gln Ser Pro Thr Thr Met Ala Ala
130 135 140

Ser Pro Gly Glu Lys Ile Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile
145 150 155 160

Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Phe Ser Pro
165 170 175

Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Gly
195 200 205

Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Gly Ser

43/48

210

215

220

Ser Ile Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys

225

230

235

<210> 74

<211> 744

<212> DNA

<213> Mus sp.

<400> 74

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggctgggac ttcagtgaag 60
atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120
aggcctggac atggacttga gtggattgga gatatttcc ctgaaagtgg taatatccac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaatcttc gagcacagcc 240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctccctca 360
ggtggtggtg gttctggcg cgccggctcc ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcaagagtc tgtaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
ccagggcagc ctcctaaact gttgatctac tggcatcca ctggaaatc tgggtccct 600
gatcgcttca caggcagtgg atctggaaca gatccactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagtttta ttactgtcag aatgattata gttatccgct cacgttcgg 720
gctgggacca agcttgagat caaa 744

<210> 75

<211> 248

<212> PRT

<213> Mus sp.

<400> 75

44/48

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly

1

5

10

15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn

20

25

30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp

35

40

45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys

50

55

60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala

65

70

75

80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe

85

90

95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser

130

135

140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser

145

150

155

160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp

165

170

175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala

180

185

190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly

195

200

205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu

210

215

220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly

225

230

235

240

Ala Gly Thr Lys Leu Glu Ile Lys

245

<210> 76

<211> 744

<212> DNA

<213> Mus sp.

<400> 76

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctggac ttcagtgaag 60

atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggttaagcag 120

aggcctggac atggacttga atgggttgaa gatatttcc ctggaagtgg taatgctcac 180

tacaatgaga agttcaaggg caaagccaca ctgactgcag acaagtccctc gtacacagcc 240

tatatgcagc tcagtagcct gacatctgag gactctgctg tctatttctg tgcaagattg 300
cggaactggg acgaggctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtgtggtg gttctggcg cgccggctcc ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat ctccttgc tatgtcagta ggacagaagg tcactatgag ctgcaagtcc 480
agtcagagcc ttttaatag tagcaatcaa aagaactatt tggcctggta ccagcagaaa 540
caagggcagc ctcctaaact gcttatctat ggggcatcca ttagagaatc ttgggtccct 600
gatcgattca caggaagtgg atctggaca gacttcactc tcaccatcag cagtgtgaag 660
gctgaagacc tggcagtttta ttactgtcag caatattata gctatccgta cacgttcgga 720
ggggggacca agcttgagat caaa 744

<210> 77

<211> 248

<212> PRT

<213> Mus sp.

<400> 77

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

85

90

95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser

130

135

140

Ser Leu Ala Met Ser Val Gly Gln Lys Val Thr Met Ser Cys Lys Ser

145

150

155

160

Ser Gln Ser Leu Leu Asn Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp

165

170

175

Tyr Gln Gln Lys Gln Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala

180

185

190

Ser Ile Arg Glu Ser Trp Val Pro Asp Arg Phe Thr Gly Ser Gly Ser

195

200

205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala Glu Asp Leu

210

215

220

Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Tyr Thr Phe Gly

48/48

225

230

235

240

Gly Gly Thr Lys Leu Glu Ile Lys

245